



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/744,910
Source: PT/09
Date Processed by STIC: 3/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/744,910

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 ☐ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)
- 12 ☐ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/744,910

DATE: 03/07/2001
 TIME: 15:23:53

Input Set : A:\es.txt
 Output Set: N:\CRF3\03072001\I744910.raw

Does Not Comply
 Corrected Diskette Needed

OK
 3 <110> APPLICANT: ASAHIKASEI KOGYO KABUSIKI KAISHA
 5 <120> TITLE OF INVENTION: Antibodies for Detecting Microorganisms
 7 <130> FILE REFERENCE: ASAHI-2
 9 <140> CURRENT APPLICATION NUMBER: US/09/744,910
 9 <141> CURRENT FILING DATE: 2001-02-01
 9 <150> PRIOR APPLICATION NUMBER: JP 10/230204
 W--> 10 <151> PRIOR FILING DATE: 1998-7-31
 12 <160> NUMBER OF SEQ ID NOS: 22

1998-07-31

↑ add φ

ERRORED SEQUENCES

52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 123
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Haemophilus influenzae
 57 <400> SEQUENCE: 2
 58 Met Ser Leu Thr Asn Glu Gln Ile Ile Glu Ala Ile Ala Ser Lys Thr
 E--> 59 1 5 10 15
 60 Val Thr Glu Ile Val Glu Leu Ile Ala Ala Met Glu Glu Lys Phe Gly
 E--> 61 20 25 30
 62 Val Ser Ala Ala Ala Val Ala Ala Pro Ala Ala Gly Gly Ala
 E--> 63 35 40 45
 64 Ala Ala Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Lys Ser Ala
 E--> 65 50 55 60
 66 Gly Ala Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly
 E--> 67 65 70 75 80
 68 Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Asn
 E--> 69 85 90 95
 70 Leu Lys Glu Gly Val Ser Lys Glu Glu Ala Glu Ala Leu Lys Lys Glu
 E--> 71 100 105 110
 72 Leu Glu Glu Ala Gly Ala Glu Val Glu Val Lys
 E--> 73 115 120
 113 <210> SEQ ID NO: 4
 114 <211> LENGTH: 125
 115 <212> TYPE: PRT
 116 <213> ORGANISM: Helicobacter pylori
 118 <400> SEQUENCE: 4
 119 Met Ala Ile Ser Lys Glu Glu Val Leu Glu Tyr Ile Gly Ser Leu Ser
 E--> 120 1 5 10 15
 121 Val Leu Glu Leu Ser Glu Leu Val Lys Met Phe Glu Glu Lys Phe Gly
 E--> 122 20 25 30
 123 Val Ser Ala Thr Pro Thr Val Val Ala Gly Ala Ala Val Ala Gly Gly
 E--> 124 35 40 45
 125 Ala Ala Ala Glu Ser Glu Glu Lys Thr Glu Phe Asn Val Ile Leu Ala
 E--> 126 50 55 60
 127 Asp Ser Gly Ala Glu Lys Ile Lys Val Ile Lys Val Val Arg Glu Ile

misaligned amino acid
 numbers - see item 4
 on Error Summary Sheet

same error

RAW SEQUENCE LISTING

DATE: 03/07/2001

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Input Set : A:\es.txt

Output Set: N:\CRF3\03072001\I744910.raw

```

E--> 128 65          70          75          80
      129 Thr Gly Leu Gly Leu Lys Glu Ala Lys Asp Ala Thr Glu Lys Thr Pro
E--> 130          85          90          95
      131 His Val Leu Lys Glu Gly Val Asn Lys Glu Glu Ala Glu Thr Ile Lys
E--> 132          100         105         110
      133 Lys Lys Leu Glu Glu Val Gly Ala Lys Val Glu Val Lys
E--> 134          115         120         125
      174 <210> SEQ ID NO: 6
      175 <211> LENGTH: 122
      176 <212> TYPE: PRT
      177 <213> ORGANISM: Streptococcus pneumoniae
      179 <400> SEQUENCE: 6
      180 Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu Ile Lys Glu Ala Ser
E--> 181 1          5          10          15
      182 Ile Leu Glu Leu Asn Asp Leu Val Lys Ala Ile Glu Glu Glu Phe Gly
E--> 183          20          25          30
      184 Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Asp Ala Ala Asp
E--> 185          35          40          45
      186 Ala Gly Ala Ala Lys Asp Ser Phe Asp Val Glu Leu Thr Ser Ala Gly
E--> 187          50          55          60
      188 Asp Lys Lys Val Gly Val Ile Lys Val Val Arg Glu Ile Thr Gly Leu
E--> 189 65         70         75         80
      190 Gly Leu Lys Glu Ala Lys Glu Leu Val Asp Gly Ala Pro Ala Leu Val
E--> 191          85          90          95
      192 Lys Glu Gly Val Ala Thr Ala Glu Ala Glu Glu Ile Lys Ala Lys Leu
E--> 193          100         105         110
      194 Glu Glu Ala Gly Ala Ser Val Thr Leu Lys
E--> 195          115         120
      235 <210> SEQ ID NO: 8
      236 <211> LENGTH: 123
      237 <212> TYPE: PRT
      238 <213> ORGANISM: Neisseria gonorrhoeae
      240 <400> SEQUENCE: 8
      241 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
E--> 242 1          5          10          15
      243 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
E--> 244          20          25          30
      245 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
E--> 246          35          40          45
      247 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
E--> 248          50          55          60
      249 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
E--> 250 65         70         75         80
      251 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
E--> 252          85          90          95
      253 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
E--> 254          100         105         110
      255 Leu Glu Ala Ala Gly Ala Lys Val Glu Ile Lys
E--> 256          115         120

```

*same**same**same*

RAW SEQUENCE LISTING

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Input Set : A:\es.txt

Output Set: N:\CRF3\03072001\I744910.raw

296 <210> SEQ ID NO: 10
 297 <211> LENGTH: 123
 298 <212> TYPE: PRT
 299 <213> ORGANISM: Neisseria meningitidis
 301 <400> SEQUENCE: 10
 302 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
 E--> 303 1 5 10 15
 304 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
 E--> 305 20 25 30
 306 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
 E--> 307 35 40 45
 308 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
 E--> 309 50 55 60
 310 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
 E--> 311 65 70 75 80
 312 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
 E--> 313 85 90 95
 314 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
 E--> 315 100 105 110
 316 Leu Glu Glu Ala Gly Ala Lys Val Glu Ile Lys
 E--> 317 115 120
 319 <210> SEQ ID NO: 11
 320 <211> LENGTH: 31
 321 <212> TYPE: DNA
 322 <213> ORGANISM: artificial sequence
 324 <220> FEATURE:
 325 <223> OTHER INFORMATION: The primers DNA for PCR used to acquire the ribosomal protein L7/L12 gene
 326 from H. influenzae.
 328 <400> SEQUENCE: 11
 E--> 329 gtaaggatcc atgtcattaa ctaacgaaca a_@_@_@_@_1
 367 <210> SEQ ID NO: 15
 368 <211> LENGTH: 31
 369 <212> TYPE: DNA
 370 <213> ORGANISM: artificial sequence
 372 <220> FEATURE:
 373 <223> OTHER INFORMATION: The primers DNA for PCR used to acquire the ribosomal protein L7/L12 gene
 374 from N. gonorrhoeae.
 376 <400> SEQUENCE: 15
 E--> 377 gtaaggatcc @ctggctatta @ctaaagaaga @_@_@_@_1
 429 <210> SEQ ID NO: 18
 430 <211> LENGTH: 123
 431 <212> TYPE: PRT
 432 <213> ORGANISM: Haemophilus influenzae
 434 <400> SEQUENCE: 18
 435 Met Ser Leu Thr Asn Glu Gln Ile Ile Glu Ala Ile Ala Ser Lys Thr
 E--> 436 1 5 10 15
 437 Val Thr Glu Ile Val Glu Leu Ile Ala Ala Met Glu Glu Lys Phe Gly
 E--> 438 20 25 30
 439 Val Ser Ala Ala Ala Val Ala Ala Ala Pro Ala Ala Gly Gly Ala

*same**delete - do not use these - they are invalid characters**delete - same error**misaligned amino acid nos.*

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Input Set : A:\es.txt
 Output Set: N:\CRF3\03072001\I744910.raw

E--> 440 35 40 45
 441 Ala Ala Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Lys Ser Ala
 E--> 442 50 55 60
 443 Gly Ala Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly
 E--> 444 65 70 75 80
 445 Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Asn
 E--> 446 85 90 95
 447 Leu Lys Glu Gly Val Ser Lys Glu Glu Ala Glu Ala Leu Lys Lys Glu
 E--> 448 100 105 110
 449 Leu Glu Glu Ala Gly Ala Glu Val Glu Val Lys
 E--> 450 115 120
 490 <210> SEQ ID NO: 20
 491 <211> LENGTH: 122
 492 <212> TYPE: PRT
 493 <213> ORGANISM: Streptococcus pneumoniae
 495 <400> SEQUENCE: 20
 496 Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu Ile Lys Glu Ala Ser
 E--> 497 1 5 10 15
 498 Ile Leu Glu Leu Asn Asp Leu Val Lys Ala Ile Glu Glu Glu Phe Gly
 E--> 499 20 25 30
 500 Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Asp Ala Ala Asp
 E--> 501 35 40 45
 502 Ala Gly Ala Ala Lys Asp Ser Phe Asp Val Glu Leu Thr Ser Ala Gly
 E--> 503 50 55 60
 504 Asp Lys Lys Val Gly Val Ile Lys Val Val Arg Glu Ile Thr Gly Leu
 E--> 505 65 70 75 80
 506 Gly Leu Lys Glu Ala Lys Glu Leu Val Asp Gly Ala Pro Ala Leu Val
 E--> 507 85 90 95
 508 Lys Glu Gly Val Ala Thr Ala Glu Ala Glu Glu Ile Lys Ala Lys Leu
 E--> 509 100 105 110
 510 Glu Glu Ala Gly Ala Ser Val Thr Leu Lys
 E--> 511 115 120
 551 <210> SEQ ID NO: 22
 552 <211> LENGTH: 123
 553 <212> TYPE: PRT
 554 <213> ORGANISM: Neisseria gonorrhoeae
 556 <400> SEQUENCE: 22
 557 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
 E--> 558 1 5 10 15
 559 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
 E--> 560 20 25 30
 561 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
 E--> 562 35 40 45
 563 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
 E--> 564 50 55 60
 565 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
 E--> 566 65 70 75 80
 567 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
 E--> 568 85 90 95

same error

same

same

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Input Set : A:\es.txt
Output Set: N:\CRF3\03072001\I744910.raw

569 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
E--> 570 100 105 110
571 Leu Glu Ala Ala Gly Ala Lys Val Glu Ile Lys
E--> 572 115 120
E--> 574 20
E--> 577 1
578

/21

same
delete at end of file

VERIFICATION SUMMARY

DATE: 03/07/2001

PATENT APPLICATION: US/09/744,910

TIME: 15:23:54

Input Set : A:\es.txt

Output Set: N:\CRF3\03072001\I744910.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:22 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:120 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:181 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:266 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9

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Input Set : A:\es.txt

Output Set: N:\CRF3\03072001\I744910.raw

L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:290 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:303 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:329 M:254 E: No. of Bases conflict, LENGTH:Input:31 Counted:39 SEQ:11
L:329 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:329 M:252 E: No. of Seq. differs, <211>LENGTH:Input:31 Found:39 SEQ:11
L:377 M:254 E: No. of Bases conflict, LENGTH:Input:31 Counted:43 SEQ:15
L:377 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:377 M:252 E: No. of Seq. differs, <211>LENGTH:Input:31 Found:43 SEQ:15
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:436 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
M:332 Repeated in SeqNo=18
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:497 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
M:332 Repeated in SeqNo=20
L:558 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
M:332 Repeated in SeqNo=22